
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=10; day=17; hr=7; min=40; sec=41; ms=10;]

Reviewer Comments:

<210> 8

<211> 31

<212> DNA

<213> Artifical Sequence

<400> 8

cacgctgtttggcatcgacctgaccatcatg

<210> 9

<211> 31

<212> DNA

<213> Artifical Sequence

<400> 9

Gccacggcacgcggaatgtgatgccgccc

Please change "Artifical" to "Artificial" in the response for numeric identifier <213>.

For SEQ ID # 8 and 9, when using "Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is made in the laboratory, please indicate that the sequence is synthesized. Please

make all necessary changes.

For SEQ ID # 8 and 9, the nucleic acid sequence is not in the proper format. Nucleotide bases must be in groups of ten nucleotides. The individual groups of ten nucleotides must be separated by a space. The sequence rules require that "the enumeration of nucleotide bases shall start at the first base of the sequence with 1. The enumeration shall be continuous through the whole sequence in the direction 5' to 3'. The enumeration shall be marked in the right margin, next to the line containing the one-letter codes for bases, and giving the number of the last base of that line." Please make all necessary changes.

Validated By CRFValidator v 1.0.3

Application No: 10553097 Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-15 14:45:15.073 **Finished:** 2008-10-15 14:45:15.670

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 597 ms

Total Warnings: 2
Total Errors: 2

No. of SeqIDs Defined: 9

Actual SeqID Count: 9

Eri	or code	Error Description
W	402	Undefined organism found in <213> in SEQ ID (8)
E	254	The total number of bases conflicts with running total Input: 0 Calculated: 31 SEQID(8)
W	402	Undefined organism found in <213> in SEQ ID (9)
E	254	The total number of bases conflicts with running total Input: 0 Calculated: 31 SEQID(9)

SEQUENCE LISTING

<110>	National R	denewable E	nergy Lal	ooratory				
<120>	OXYGEN RES	SISTANT HYD	ROGENASES	S AND MET	THODS FOR	R DESIGN	ING AND MA	KING SAME
<130>	NREL 03-11							
<140> <141>	10553097 2008-10-15	·						
<160>	9							
<170>	PatentIn v	ersion 3.4						
<210><211><211><212><213>	1 333 PRT Chlamydomo	onas reinha	rdtii					
<400>	1							
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Ala Le	u Asn Asp P 20	ro Lys Lys	His Val 25	Ile Val	Ala Met	Ala Pro 30	Ser	
Val Ar	g Thr Ala M 35	Iet Gly Glu	Leu Phe	Lys Met	Gly Tyr 45	Gly Lys	Asp	
Val Th	r Gly Lys L	eu Tyr Thr 55		-	Leu Gly	Phe Asp	Lys	
Val Ph	e Asp Ile A	sn Phe Gly 70	Ala Asp	Met Thr 75	Ile Met	Glu Glu	Ala 80	
Thr Gl	u Leu Leu G 8	ly Arg Val 5	Lys Asn	Asn Gly	Pro Phe	Pro Met 95	Phe	
Thr Se	r Cys Cys P 100	ro Ala Trp	Val Arg 105	Leu Ala	Gln Asn	Tyr His	Pro	
Glu Le	u Leu Asp A 115	sn Leu Ser	Ser Ala	Lys Ser	Pro Gln 125	Gln Ile	Phe	

Gly Thr Ala Ser Lys Thr Tyr Tyr Pro Ser Ile Ser Gly Ile Ala Pro

140

135

130

Glu Asp Val Tyr Thr Val Thr Ile Met Pro Cys Asn Asp Lys Lys Tyr 150 Glu Ala Asp Ile Pro Phe Met Glu Thr Asn Ser Leu Arg Asp Ile Asp 170 175 165 Ala Ser Leu Thr Thr Arg Glu Leu Ala Lys Met Ile Lys Asp Ala Lys 190 180 185 Ile Lys Phe Ala Asp Leu Glu Asp Gly Glu Val Asp Pro Ala Met Gly 200 205 195 Thr Tyr Ser Gly Ala Gly Ala Ile Phe Gly Ala Thr Gly Gly Val Met 215 Glu Ala Ile Arg Ser Ala Lys Asp Phe Ala Glu Asn Lys Glu Leu 225 230 235 Glu Asn Val Asp Tyr Thr Glu Val Arg Gly Phe Lys Gly Ile Lys Glu 245 250 255 Ala Glu Val Glu Ile Ala Gly Asn Lys Leu Asn Val Ala Val Ile Asn 2.65 260 270 Gly Ala Ser Asn Phe Phe Glu Phe Met Lys Ser Gly Lys Met Asn Glu 275 280 285 Lys Gln Tyr His Phe Ile Glu Val Met Ala Cys Pro Gly Gly Cys Ile 290 295 300 Asn Gly Gly Gln Pro His Val Asn Ala Leu Asp Arg Glu Asn Val 305 310 315 320 Asp Tyr Arg Lys Leu Arg Ala Ser Val Leu Tyr Asn Gln 325 330 <210> 2

<400> 2

<211> 333 <212> PRT

<213> Chlamydomonas reinhardtii

Pro 1	Val	Ala	Ala	Leu 5	Ser	Glu	Lys	Ser	His 10	Met	Asp	Arg	Val	Lys 15	Asn
Ala	Leu	Asn	Ala 20	Pro	Glu	Lys	His	Val 25	Ile	Val	Ala	Met	Ala 30	Pro	Ser
Val	Arg	Ala 35	Ser	Ile	Gly	Glu	Leu 40	Phe	Asn	Met	Gly	Phe 45	Gly	Val	Asp
Val	Thr 50	Gly	Lys	Ile	Tyr	Thr 55	Ala	Leu	Arg	Gln	Leu 60	Gly	Phe	Asp	Lys
Ile 65	Phe	Asp	Ile	Asn	Phe 70	Gly	Ala	Asp	Met	Thr 75	Ile	Met	Glu	Glu	Ala 80
Thr	Glu	Leu	Val	Gln 85	Arg	Ile	Glu	Asn	Asn 90	Gly	Pro	Phe	Pro	Met 95	Phe
Thr	Ser	Суз	Cys 100	Pro	Gly	Trp	Val	Arg 105	Gln	Ala	Glu	Asn	Tyr 110	Tyr	Pro
Glu	Leu	Leu 115	Asn	Asn	Leu	Ser	Ser 120	Ala	Lys	Ser	Pro	Gln 125	Gln	Ile	Phe
Gly	Thr 130	Ala	Ser	Lys	Thr	Tyr 135	Tyr	Pro	Ser	Ile	Ser 140	Gly	Leu	Asp	Pro
Lys 145	Asn	Val	Phe	Thr	Val 150	Thr	Val	Met	Pro	Cys 155	Thr	Ser	Lys	Lys	Phe 160
Glu	Ala	Asp	Arg	Pro 165	Gln	Met	Glu	Lys	Asp 170	Gly	Leu	Arg	Asp	Ile 175	Asp
Ala	Val	Ile	Thr 180	Thr	Arg	Glu	Leu	Ala 185	Lys	Met	Ile	Lys	Asp 190	Ala	Lys
Ile	Pro	Phe 195	Ala	Lys	Leu	Glu	Asp 200	Ser	Glu	Ala	Asp	Pro 205	Ala	Met	Gly
Glu	Tyr 210	Ser	Gly	Ala	Gly	Ala 215	Ile	Phe	Gly	Ala	Thr 220	Gly	Gly	Val	Met

Glu Ala Ala Leu Arg Ser Ala Lys Asp Phe Ala Glu Asn Ala Glu Leu

225 230 235 240

Glu Asp Ile Glu Tyr Lys Gln Val Arg Gly Leu Asn Gly Ile Lys Glu
245 250 255

Ala Glu Val Glu Ile Asn Asn Asn Lys Tyr Asn Val Ala Val Ile Asn 260 265 270

Gly Ala Ser Asn Leu Phe Lys Phe Met Lys Ser Gly Met Ile Asn Glu 275 280 285

Lys Gln Tyr His Phe Ile Glu Val Met Ala Cys His Gly Gly Cys Val 290 295 300

Asn Gly Gly Gln Gln Pro His Val Asn Pro Lys Asp Leu Glu Lys Val 305 310 315 320

Asp Ile Lys Lys Val Arg Ala Ser Val Leu Tyr Asn Gln 325 330

<210> 3

<211> 321

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 3

Pro Glu Asn Ala Ile Tyr Glu Ala Gln Ser Trp Val Pro Glu Val Glu

1 5 10 15

Lys Lys Leu Lys Asp Gly Lys Val Lys Cys Ile Ala Met Pro Ala Pro 20 25 30

Ala Val Arg Tyr Ala Leu Gly Asp Ala Phe Gly Met Pro Val Gly Ser 35 40 45

Val Thr Thr Gly Lys Met Leu Ala Ala Leu Gln Lys Leu Gly Phe Ala 50 55 60

His Cys Trp Asp Thr Glu Phe Thr Ala Asp Val Thr Ile Trp Glu Glu 65 70 75 80

Gly Ser Glu Phe Val Glu Arg Leu Thr Lys Lys Ser Asp Met Pro Leu 85 90 95

Pro	Gln	Phe	Thr 100	Ser	Cys	Суз	Pro	Gly 105	Trp	Gln	Lys	Tyr	Ala 110	Glu	Thr
Tyr	Tyr	Pro 115	Glu	Leu	Leu	Pro	His 120	Phe	Ser	Thr	Cys	Lys 125	Ser	Pro	Ile
Gly	Met 130	Asn	Gly	Ala	Leu	Ala 135	Lys	Thr	Tyr	Gly	Ala 140	Glu	Arg	Met	Lys
Tyr 145	Asp	Pro	Lys	Gln	Val 150	Tyr	Thr	Val	Ser	Ile 155	Met	Pro	Суз	Ile	Ala 160
Lys	Lys	Tyr	Glu	Gly 165	Leu	Arg	Pro	Glu	Leu 170	Lys	Ser	Ser	Gly	Met 175	Arg
Asp	Ile	Asp	Ala 180	Thr	Leu	Thr	Thr	Arg 185	Glu	Leu	Ala	Tyr	Met 190	Ile	Lys
Lys	Ala	Gly 195	Ile	Asp	Phe	Ala	Lys 200	Leu	Pro	Asp	Gly	Lys 205	Arg	Asp	Ser
Leu	Met 210	Gly	Glu	Ser	Thr	Gly 215	Gly	Ala	Thr	Ile	Phe 220	Gly	Val	Thr	Gly
Gly 225	Val	Met	Glu	Ala	Ala 230	Leu	Arg	Phe	Ala	Tyr 235	Glu	Ala	Val	Thr	Gly 240
Lys	Lys	Pro	Asp	Ser 245	Trp	Asp	Phe	Lys	Ala 250	Val	Arg	Gly	Leu	Asp 255	Gly
Ile	Lys	Glu	Ala 260	Thr	Val	Asn	Val	Gly 265	Gly	Thr	Asp	Val	Lys 270	Val	Ala
		275	Gly		_		280	_			_	285			
Ala	Gly 290	Lys	Ser	Pro	Tyr	His 295	Phe	Ile	Glu	Tyr	Met 300	Ala	Cys	Pro	Gly
Gly 305	Суз	Val	Cys	Gly	Gly 310	Gly	Gln	Pro	Val	Met 315	Pro	Gly	Val	Leu	Glu 320

<210> 4 <211> 393 <212> PRT <213> Chlamydomonas reinhardtii <400> 4 Ala Thr Asp Ala Val Pro His Trp Lys Leu Ala Leu Glu Glu Leu Asp Lys Pro Lys Asp Gly Gly Arg Lys Val Leu Ile Ala Gln Val Ala Pro 20 25 Ala Val Arg Val Ala Ile Ala Glu Ser Phe Gly Leu Ala Pro Gly Ala 35 40 45 Val Ser Pro Gly Lys Leu Ala Ala Gly Leu Arg Ala Leu Gly Phe Asp 55 Gln Val Phe Asp Thr Leu Phe Ala Ala Asp Leu Thr Ile Met Glu Glu 70 75 Gly Thr Glu Leu Leu His Arg Leu Lys Glu His Leu Glu Ala His Pro 85 90 His Ser Asp Glu Pro Leu Pro Met Phe Thr Ser Cys Cys Pro Gly Trp 100 105 110 Val Ala Met Met Glu Lys Ser Tyr Pro Glu Leu Ile Pro Phe Val Ser 115 120 125 Ser Cys Lys Ser Pro Gln Met Met Gly Ala Met Val Lys Thr Tyr 130 135 140 Leu Ser Glu Lys Gln Gly Ile Pro Ala Lys Asp Ile Val Met Val Ser 145 150 155 160 Val Met Pro Cys Val Arg Lys Gln Gly Glu Ala Asp Arg Glu Trp Phe 170 165

Cys Val Ser Glu Pro Gly Val Arg Asp Val Asp His Val Ile Thr Thr

185

190

180

Ala Glu Leu Gly Asn Ile Phe Lys Glu Arg Gly Ile Ile Leu Pro Glu 200 Leu Pro Asp Ser Asp Trp Asp Gln Pro Leu Gly Leu Gly Ser Gly Ala 215 220 210 Gly Val Leu Phe Gly Thr Thr Gly Gly Val Met Glu Ala Ala Val Arg 225 230 235 240 Thr Ala Tyr Glu Ile Val Thr Lys Glu Pro Leu Pro Arg Leu Asn Leu 245 250 255 Ser Glu Val Arg Gly Leu Asp Gly Ile Lys Glu Ala Ser Val Thr Leu 260 265 Val Pro Ala Pro Gly Ser Lys Phe Ala Glu Leu Val Ala Ala Arg Leu 275 280 285 Ala His Lys Val Glu Glu Ala Ala Ala Ala Glu Ala Ala Ala Val 290 295 300 Glu Gly Ala Val Lys Pro Pro Ile Ala Tyr Asp Gly Gly Gln Gly Phe 315 310 305 320 Ser Thr Asp Asp Gly Lys Gly Gly Leu Lys Leu Arg Val Ala Val Ala 325 330 335 Asn Gly Leu Gly Asn Ala Lys Lys Leu Ile Gly Lys Met Val Ser Gly 340 345 350 Glu Ala Lys Tyr Asp Phe Val Glu Ile Met Ala Cys Pro Ala Gly Cys 355 360 365 Val Gly Gly Gly Gln Pro Arg Ser Thr Asp Lys Gln Ile Thr Gln 380 370 375 Lys Arg Gln Ala Ala Leu Tyr Asp Leu 385 390

<210> 5 <211> 386 <212> PRT <400> 5

Ala Glu Ala Pro Leu Ser His Val Gln Gln Ala Leu Ala Glu Leu Ala 1 5 10 15

Lys Pro Lys Asp Asp Pro Thr Arg Lys His Val Cys Val Gln Val Ala 20 25 30

Pro Ala Val Arg Val Ala Ile Ala Glu Thr Leu Gly Leu Ala Pro Gly 35 40 45

Ala Thr Thr Pro Lys Gln Leu Ala Glu Gly Leu Arg Arg Leu Gly Phe 50 55 60

Asp Glu Val Phe Asp Thr Leu Phe Gly Ala Asp Leu Thr Ile Met Glu 65 70 75 80

Glu Gly Ser Glu Leu Leu His Arg Leu Thr Glu His Leu Glu Ala His
85 90 95

Pro His Ser Asp Glu Pro Leu Pro Met Phe Thr Ser Cys Cys Pro Gly
100 105 110

Trp Ile Ala Met Leu Glu Lys Ser Tyr Pro Asp Leu Ile Pro Tyr Val 115 120 125

Ser Ser Cys Lys Ser Pro Gln Met Met Leu Ala Ala Met Val Lys Ser 130 135 140

Ser Ile Met Pro Cys Thr Arg Lys Gln Ser Glu Ala Asp Arg Asp Trp 165 170 175

Phe Cys Val Asp Ala Asp Pro Thr Leu Arg Gln Leu Asp His Val Ile 180 185 190

Thr Thr Val Glu Leu Gly Asn Ile Phe Lys Glu Arg Gly Ile Asn Leu 195 200 205

Ala Glu Leu Pro Glu Gly Glu Trp Asp Asn Pro Met Gly Val Gly Ser

210 215 220

Gly Ala Gly Val Leu Phe Gly Thr Thr Gly Gly Val Met Glu Ala Ala 225 230 235 240

Leu Arg Thr Ala Tyr Glu Leu Phe Thr Gly Thr Pro Leu Pro Arg Leu 245 250 255

Ser Leu Ser Glu Val Arg Gly Met Asp Gly Ile Lys Glu Thr Asn Ile 260 265 270

Thr Met Val Pro Ala Pro Gly Ser Lys Phe Glu Glu Leu Leu Lys His 275 280 285

Arg Ala Ala Arg Ala Glu Ala Ala Ala His Gly Thr Pro Gly Pro 290 295 300

Leu Ala Trp Asp Gly Gly Ala Gly Phe Thr Ser Glu Asp Gly Arg Gly 305 310 315 320

Gly Ile Thr Leu Arg Val Ala Val Ala Asn Gly Leu Gly Asn Ala Lys 325 330 335

Lys Leu Ile Thr Lys Met Gln Ala Gly Glu Ala Lys Tyr Asp Phe Val\$340\$ \$345\$ \$350

Glu Ile Met Ala Cys Pro Ala Gly Cys Val Gly Gly Gly Gln Pro 355 360 365

Arg Ser Thr Asp Lys Ala Ile Thr Gln Lys Arg Gln Ala Ala Leu Tyr 370 375 380

Asn Leu 385

<210> 6

<211> 441

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 6

Ala Ala Pro Ala Ala Glu Ala Pro Leu Ser His Val Gln Gln Ala Leu 1 5 10 15

Ala Glu Le	eu Ala Lys 20	Pro Lys		Asp 25	Pro	Thr	Arg	Lys	His 30	Val	Cys
Val Gln Va		Ala Val	Arg 40	Val	Ala	Ile	Ala	Glu 45	Thr	Leu	Gly
Leu Ala Pi 50	ro Gly Ala	Thr Thr 55	Pro	Lys	Gln	Leu	Ala 60	Glu	Gly	Leu	Arg
Arg Leu G	ly Phe Asp	Glu Val 70	Phe	Asp	Thr	Leu 75	Phe	Gly	Ala	Asp	Leu 80
Thr Ile Me	et Glu Glu 85	Gly Ser	Glu	Leu	Leu 90	His	Arg	Leu	Thr	Glu 95	His
Leu Glu A	la His Pro 100	His Ser	_	Glu 105	Pro	Leu	Pro	Met	Phe 110	Thr	Ser
	ro Gly Trp 15	Ile Ala	Met 120	Leu	Glu	Lys	Ser	Tyr 125	Pro	Asp	Leu
Ile Pro Ty	yr Val Ser	Ser Cys 135	Lys	Ser	Pro	Gln	Met 140	Met	Leu	Ala	Ala
Met Val Ly 145	ys Ser Tyr	Leu Ala 150	Glu	Lys	Lys	Gly 155	Ile	Ala	Pro	Lys	Asp 160
Met Val Me	et Val Ser 165		Pro	Суз	Thr 170	Arg	Lys	Gln	Ser	Glu 175	Ala
Asp Arg As	sp Trp Phe 180	Cys Val	_	Ala 185	Asp	Pro	Thr	Leu	Arg 190	Gln	Leu
Asp His Va	al Ile Thr 95	Thr Val	Glu 200	Leu	Gly	Asn	Ile	Phe 205	Lys	Glu	Arg
Gly Ile As	sn Leu Ala	Glu Leu 215	Pro	Glu	Gly	Glu	Trp 220	Asp	Asn	Pro	Met